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==============================================================
Sequence Listing was accepted.
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217-9197 (toll free).
Reviewer: Keisha Douglas
Timestamp: Thu Aug 30 16:03:23 EDT 2007
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                Validated By CRFValidator v 1.0.3

Application No:        10764131              Version No:         2.0


              Input Set:


              Output Set:



                Started:  2007-08-20 08:38:33.548
               Finished:  2007-08-20 08:38:34.020
                Elapsed:  0 hr(s) 0 min(s) 0 sec(s) 472 ms
         Total Warnings:  5
           Total Errors:  0
   No. of SeqIDs Defined:  5
      Actual SeqID Count:  5
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Error code      Error Description

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W   213      Artificial or Unknown found in <213>  in SEQ ID (2)

W   213      Artificial or Unknown found in <213>  in SEQ ID (3)

W   213      Artificial or Unknown found in <213>  in SEQ ID (4)

W   213      Artificial or Unknown found in <213>  in SEQ ID (5)

<110> KELER, TIBOR
      GOLDSTEIN, JOEL
      GRAZIANO, ROBERT
      DEO, YASHWANT M.

<120> CELLS EXPRESSING ANTI-FC RECEPTOR BINDING COMPONENTS

<130> CDJ-099CN

<140>  10764131
<141>  2004-01-23


<150> 09/203,958
<151> 1998-12-02

<150> 60/067,232
<151> 1997-12-02

<160> 5

<170> PatentIn Ver. 3.3

<210> 1
<211> 1132
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      construct

<220>
<221> CDS
<222> (74)..(1129)

<400> 1
aagcttggta ccgagctcgg atccactagt aacggccgcc agtgtgctgg aattcggctt 60

gggatatcc acc atg gag aca gac aca ctc ctg cta tgg gta ctg ctg     109
                Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu
                 1               5                  10

ctc tgg gtt cca ggt tcc act ggt gac tat cca tat gat gtt cca gat   157
Leu Trp Val Pro Gly Ser Thr Gly Asp Tyr Pro Tyr Asp Val Pro Asp
         15                  20                  25

tat gct ggg gcc cag ccg gcc aga tct gat atc cag ctg acc cag agc   205
Tyr Ala Gly Ala Gln Pro Ala Arg Ser Asp Ile Gln Leu Thr Gln Ser
     30                  35                  40

cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc atc acc tgt   253
Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
 45                  50                  55                  60

```
aag tcc agt caa agt gtt tta tac agt tca aat cag aag aac tac ttg      301
Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu
                65                  70                  75


gcc tgg tac cag cag aag cca ggt aag gct cca aag ctg ctg atc tac      349
Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
                80                  85                  90


tgg gca tcc act agg gaa tct ggt gtg cca agc aga ttc agc ggt agc      397
Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
            95                  100                 105


ggt agc ggt acc gac ttc acc ttc acc atc agc agc ctc cag cca gag      445
Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu
        110                 115                 120


gac atc gcc acc tac tac tgc cat caa tac ctc tcc tcg tgg acg ttc      493
Asp Ile Ala Thr Tyr Tyr Cys His Gln Tyr Leu Ser Ser Trp Thr Phe
125                 130                 135                 140


ggc caa ggg acc aag gtg gaa atc aag agc tct ggc ggt ggc ggc tcc      541
Gly Gln Gly Thr Lys Val Glu Ile Lys Ser Ser Gly Gly Gly Gly Ser
                145                 150                 155


gga ggt gga ggc agc gga ggg ggt gga tcc gag gtc caa ctg gtg gag      589
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu
            160                 165                 170


agc ggt gga ggt gtt gtg caa cct ggc cgg tcc ctg cgc ctg tcc tgc      637
Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys
        175                 180                 185


tcc tcg tct ggc ttc att ttc agt gac aat tac atg tat tgg gtg aga      685
Ser Ser Ser Gly Phe Ile Phe Ser Asp Asn Tyr Met Tyr Trp Val Arg
        190                 195                 200


cag gca cct gga aaa ggt ctt gag tgg gtt gca acc att agt gat ggt      733
Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Thr Ile Ser Asp Gly
205                 210                 215                 220


ggt agt tac acc tac tat cca gac agt gtg aag gga aga ttt aca ata      781
Gly Ser Tyr Thr Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile
                225                 230                 235


tcg aga gac aac agc aag aac aca ttg ttc ctg caa atg gac agc ctg      829
Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe Leu Gln Met Asp Ser Leu
            240                 245                 250


aga ccc gaa gac acc ggg gtc tat ttt tgt gca aga ggc tac tat agg      877
Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys Ala Arg Gly Tyr Tyr Arg
        255                 260                 265


tac gag ggg gct atg gac tac tgg ggc caa ggg acc ccg gtc acc gtc      925
Tyr Glu Gly Ala Met Asp Tyr Trp Gly Gln Gly Thr Pro Val Thr Val
        270                 275                 280


tcc tca ccg cgg ctg cag gtc gac gaa caa aaa ctc atc tca gaa gag      973
```

```
Ser Ser Pro Arg Leu Gln Val Asp Glu Gln Lys Leu Ile Ser Glu Glu
285                 290                 295                 300


gat ctg aat gct gtg ggc cag gac acg cag gag gtc atc gtg gtg cca   1021
Asp Leu Asn Ala Val Gly Gln Asp Thr Gln Glu Val Ile Val Val Pro
                305                 310                 315


cac tcc ttg ccc ttt aag gtg gtg gtg atc tca gcc atc ctg gcc ctg   1069
His Ser Leu Pro Phe Lys Val Val Val Ile Ser Ala Ile Leu Ala Leu
                320                 325                 330


gtg gtg ctc acc atc atc tcc ctt atc atc ctc atc atg ctt tgg cag   1117
Val Val Leu Thr Ile Ile Ser Leu Ile Ile Leu Ile Met Leu Trp Gln
        335                 340                 345


aag aag cca cgt tag                                                1132
Lys Lys Pro Arg
    350




<210> 2
<211> 1135
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      construct

<220>
<221> CDS
<222> (74)..(1132)

<400> 2
aagcttggta ccgagctcgg atccactagt aacggccgcc agtgtgctgg aattcggctt 60

ggggatatcc acc atg gag aca gac aca ctc ctg cta tgg gta ctg ctg   109
            Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu
             1               5                  10


ctc tgg gtt cca ggt tcc act ggt gac tat cca tat gat gtt cca gat   157
Leu Trp Val Pro Gly Ser Thr Gly Asp Tyr Pro Tyr Asp Val Pro Asp
        15                  20                  25


tat gct ggg gcc cag ccg gcc aga tct gag atc cag ctg cag cag act   205
Tyr Ala Gly Ala Gln Pro Ala Arg Ser Glu Ile Gln Leu Gln Gln Thr
    30                  35                  40


gga cct gag ctg gtg aag cct ggg gct tca gtg aag ata tcc tgc aag   253
Gly Pro Glu Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys
 45                  50                  55                  60


gct tct ggt tat tca ttc act gac tac atc ata ttt tgg gtg aag cag   301
Ala Ser Gly Tyr Ser Phe Thr Asp Tyr Ile Ile Phe Trp Val Lys Gln
                65                  70                  75


agc cat gga aag agc ctt gag tgg act gga aat att aat cct tac tat   349
```

```
Ser His Gly Lys Ser Leu Glu Trp Thr Gly Asn Ile Asn Pro Tyr Tyr
            80                  85                  90


ggt agt act agc tac aat ctg aag ttc aag ggc aag gcc aca ttg act   397
Gly Ser Thr Ser Tyr Asn Leu Lys Phe Lys Gly Lys Ala Thr Leu Thr
            95                  100                 105


gta gac aaa tct tcc agc aca gcc tac atg cag ctc aac agt ctg aca   445
Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Asn Ser Leu Thr
    110                 115                 120


tct gag gac tct gca gtc tat tac tgt gta aga gga gtt tat tac tac   493
Ser Glu Asp Ser Ala Val Tyr Tyr Cys Val Arg Gly Val Tyr Tyr Tyr
125                 130                 135                 140


ggt agt agc tac gag gcg ttt cct tac tgg ggc caa ggg act ctg gtc   541
Gly Ser Ser Tyr Glu Ala Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val
                    145                 150                 155


act gtc tct gca gga ggt ggc ggc tcc gga gga ggt ggc agc gga ggg   589
Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
            160                 165                 170


ggc gga tcc gat gtt gtg atg acc cag act cca ctc act ttg tcg att   637
Gly Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser Ile
            175                 180                 185


acc att gga caa cca gcc tcc atc tct tgc aag tca agt cag agc ctc   685
Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu
            190                 195                 200


tta gat agt gat gga aag aca tat ttg aat tgg ttg tta cag agg cca   733
Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro
205                 210                 215                 220


ggc cag tct cca acg cgc cta atc tat ctg gtg tct aaa ctg gac tct   781
Gly Gln Ser Pro Thr Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser
                    225                 230                 235


gga gtc cct gac agg ttc act ggc agt gga tca ggg aca gat ttc aca   829
Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr
                    240                 245                 250


ctg aaa atc agc aga gtg gag gct gag gat ttg gga att tat tat tgc   877
Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Ile Tyr Tyr Cys
            255                 260                 265


tgg caa ggt gca cat ttt cct cag acg ttc ggt gga ggc acc aag ctg   925
Trp Gln Gly Ala His Phe Pro Gln Thr Phe Gly Gly Gly Thr Lys Leu
            270                 275                 280


gaa atc aaa ccg cgg ctg cag gtc gac gaa caa aaa ctc atc tca gaa   973
Glu Ile Lys Pro Arg Leu Gln Val Asp Glu Gln Lys Leu Ile Ser Glu
285                 290                 295                 300


gag gat ctg aat gct gtg ggc cag gac acg cag gag gtc atc gtg gtg   1021
Glu Asp Leu Asn Ala Val Gly Gln Asp Thr Gln Glu Val Ile Val Val
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```
cca cac tcc ttg ccc ttt aag gtg gtg gtg atc tca gcc atc ctg gcc    1069
Pro His Ser Leu Pro Phe Lys Val Val Val Ile Ser Ala Ile Leu Ala
            320                   325                   330

ctg gtg gtg ctc acc atc atc tcc ctt atc atc ctc atc atg ctt tgg    1117
Leu Val Val Leu Thr Ile Ile Ser Leu Ile Ile Leu Ile Met Leu Trp
            335                   340                   345

cag aag aag cca cgt tag                                             1135
Gln Lys Lys Pro Arg
        350
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<210> 3
<211> 352
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      construct

<400> 3
Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
  1               5                  10                  15

Gly Ser Thr Gly Asp Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Ala
            20                  25                  30

Gln Pro Ala Arg Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu
        35                  40                  45

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ser Ser Gln
    50                  55                  60

Ser Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln
 65                  70                  75                  80

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr
                85                  90                  95

Arg Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
            100                 105                 110

Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr
            115                 120                 125

Tyr Tyr Cys His Gln Tyr Leu Ser Ser Trp Thr Phe Gly Gln Gly Thr
        130                 135                 140

Lys Val Glu Ile Lys Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
145                 150                 155                 160

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
                165                 170                 175
```

Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ser Ser Ser Gly
            180                 185                 190

Phe Ile Phe Ser Asp Asn Tyr Met Tyr Trp Val Arg Gln Ala Pro Gly
            195                 200                 205

Lys Gly Leu Glu Trp Val Ala Thr Ile Ser Asp Gly Gly Ser Tyr Thr
            210                 215                 220

Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
225                 230                 235                 240

Ser Lys Asn Thr Leu Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp
            245                 250                 255

Thr Gly Val Tyr Phe Cys Ala Arg Gly Tyr Tyr Arg Tyr Glu Gly Ala
            260                 265                 270

Met Asp Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Pro Arg
            275                 280                 285

Leu Gln Val Asp Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ala
            290                 295                 300

Val Gly Gln Asp Thr Gln Glu Val Ile Val Val Pro His Ser Leu Pro
305                 310                 315                 320

Phe Lys Val Val Val Ile Ser Ala Ile Leu Ala Leu Val Val Leu Thr
            325                 330                 335

Ile Ile Ser Leu Ile Ile Leu Ile Met Leu Trp Gln Lys Lys Pro Arg
            340                 345                 350


<210> 4
<211> 353
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      construct

<400> 4
Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
  1               5                  10                  15

Gly Ser Thr Gly Asp Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Ala
            20                  25                  30

Gln Pro Ala Arg Ser Glu Ile Gln Leu Gln Gln Thr Gly Pro Glu Leu
            35                  40                  45

Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr
    50                  55                  60

Ser Phe Thr Asp Tyr Ile Ile Phe Trp Val Lys Gln Ser His Gly Lys
65                  70                  75                  80

Ser Leu Glu Trp Thr Gly Asn Ile Asn Pro Tyr Tyr Gly Ser Thr Ser
                85                  90                  95

Tyr Asn Leu Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser
            100                 105                 110

Ser Ser Thr Ala Tyr Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser
            115                 120                 125

Ala Val Tyr Tyr Cys Val Arg Gly Val Tyr Tyr Tyr Gly Ser Ser Tyr
        130                 135                 140

Glu Ala Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
145                 150                 155                 160

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
                165                 170                 175

Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser Ile Thr Ile Gly Gln
            180                 185                 190

Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser Asp
            195                 200                 205

Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro Gly Gln Ser Pro
    210                 215                 220

Thr Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro Asp
225                 230                 235                 240

Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser
            245                 250                 255

Arg Val Glu Ala Glu Asp Leu Gly Ile Tyr Tyr Cys Trp Gln Gly Ala
            260                 265                 270

His Phe Pro Gln Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Pro
    275                 280                 285

Arg Leu Gln Val Asp Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
    290                 295                 300

Ala Val Gly Gln Asp Thr Gln Glu Val Ile Val Val Pro His Ser Leu
305                 310                 315                 320

Pro Phe Lys Val Val Val Ile Ser Ala Ile Leu Ala Leu Val Val Leu
            325                 330                 335

Thr Ile Ile Ser Leu Ile Ile Leu Ile Met Leu Trp Gln Lys Lys Pro
            340                 345                 350

Arg

<210> 5
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 5
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
  1               5                  10                  15